

0570  
0409

OPIE

## RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/10/099,704

TIME: 15:53:59

Input Set : N:\CrF3\RULE60\10099704.raw

Output Set: N:\CRF3\04162002\J099704.raw

1 <110> APPLICANT: Christensen, Bjorn Eggert  
 2 Mollgaard, Henrik  
 3 Kaasgaard, Svend  
 4 Lehmbeck, Jan  
 5 <120> TITLE OF INVENTION: Methods for producing polypeptides in  
 6 aspergillus mutant cells  
 7 <130> FILE REFERENCE: 4483.200-US  
 8 <140> CURRENT APPLICATION NUMBER: 10/099,704  
 9 <141> CURRENT FILING DATE: 2002-03-15  
 11 <150> PRIOR APPLICATION NUMBER: 09/472,364  
 12 <151> PRIOR FILING DATE: 1999-12-23  
 15 <150> PRIOR APPLICATION NUMBER: 60/139,593  
 16 <151> PRIOR FILING DATE: 1999-06-17  
 17 <150> PRIOR APPLICATION NUMBER: 60/117,396  
 18 <151> PRIOR FILING DATE: 1999-01-27  
 19 <150> PRIOR APPLICATION NUMBER: PA 1999 00745  
 20 <151> PRIOR FILING DATE: 1999-05-27  
 21 <150> PRIOR APPLICATION NUMBER: PA 1998 01726  
 22 <151> PRIOR FILING DATE: 1998-12-23  
 23 <160> NUMBER OF SEQ ID NOS: 6  
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1393  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Primer 5956  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (15)...(1328)  
 34 <400> SEQUENCE: 1  
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 36 Met Glu Ile Ser Lys Lys Ala Ala Thr Leu Leu Pro  
 37 1 5 10  
 38 aag ccc ttc tac gtg ctg agt caa gcc ctg aac ctc tcg aac aag gac 98  
 39 Lys Pro Phe Tyr Val Leu Ser Gln Ala Leu Asn Leu Ser Asn Lys Asp  
 40 15 20 25  
 41 cac aca aaa tgg tgg tat agc aca gct ccg atg ttt gcc acc atg atg 146  
 42 His Thr Lys Trp Trp Tyr Ser Thr Ala Pro Met Phe Ala Thr Met Met  
 43 30 35 40  
 44 gcg ggg gcc ggc tat gat gtt cac gca cag tac aag ttc ctc tgt atc 194  
 45 Ala Gly Ala Gly Tyr Asp Val His Ala Gln Tyr Lys Phe Leu Cys Ile  
 46 45 50 55 60  
 47 cac cgt gag gtc atc atc ccg gcg ttg ggt cca tac cca gaa aag ggt 242

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48	His Arg Glu Val Ile Ile Pro Ala Leu Gly Pro Tyr Pro Glu Lys Gly	
49		65 70 75
50	cag ccc atg cac tgg aag agt cat ctc aca cgc ttc gga ctt cct ttc	290
51	Gln Pro Met His Trp Lys Ser His Leu Thr Arg Phe Gly Leu Pro Phe	
52		80 85 90
53	gag ctg agc ttc aat tac tcc aaa tca cta cta cgg ttt gca ttc gag	338
54	Glu Leu Ser Phe Asn Tyr Ser Lys Ser Leu Leu Arg Phe Ala Phe Glu	
55		95 100 105
56	ccc ctc ggt tcc ctg acg gga acg aag gat gat cca ttc aac acc cag	386
57	Pro Leu Gly Ser Leu Thr Gly Thr Lys Asp Asp Pro Phe Asn Thr Gln	
58		110 115 120
59	gca atc agg cct gtt ctc cag gac ctc aag gcc atg gtt cca ggg ctt	434
60	Ala Ile Arg Pro Val Leu Gln Asp Leu Lys Ala Met Val Pro Gly Leu	
61		125 130 135 140
62	gac ctg gaa tgg ttc gat cat ttc act aaa gca ttg gtc gtt tcg gag	482
63	Asp Leu Glu Trp Phe Asp His Phe Thr Lys Ala Leu Val Val Ser Glu	
64		145 150 155
65	gaa gag gct cgg act ctg cta gat cga gat att gag atc ccc gtc ttc	530
66	Glu Glu Ala Arg Thr Leu Leu Asp Arg Asp Ile Glu Ile Pro Val Phe	
67		160 165 170
68	aag aca cag aac aaa ctg gca gcc gat ctg gag cca tct ggc gat att	578
69	Lys Thr Gln Asn Lys Leu Ala Ala Asp Leu Glu Pro Ser Gly Asp Ile	
70		175 180 185
71	gtc ttg aag acc tac atc tac ccg cgg atc aag tcg atc gcg acc ggg	626
72	Val Leu Lys Thr Tyr Ile Tyr Pro Arg Ile Lys Ser Ile Ala Thr Gly	
73		190 195 200
74	acc cca aaa gag aga ctc atg ttt gac gca atc aag gct gcc gac aag	674
75	Thr Pro Lys Glu Arg Leu Met Phe Asp Ala Ile Lys Ala Ala Asp Lys	
76		205 210 215 220
77	ttt ggc aaa gtt gcc act cca ctg gca atc ctc gag gag ttt ata gct	722
78	Phe Gly Lys Val Ala Thr Pro Leu Ala Ile Leu Glu Glu Phe Ile Ala	
79		225 230 235
80	gag cga gca ccc acc ctc ctc ggc cac ttt ctc tca tgc gat ttg gtc	770
81	Glu Arg Ala Pro Thr Leu Leu Gly His Phe Leu Ser Cys Asp Leu Val	
82		240 245 250
83	aag ccg tcc gag tcc cga atc aag gtc tac tgt atg gaa cgc cag ctc	818
84	Lys Pro Ser Glu Ser Arg Ile Lys Val Tyr Cys Met Glu Arg Gln Leu	
85		255 260 265
86	gac ctg gcc tcc atc gaa ggt att tgg act ctc aac ggg cga cgg aac	866
87	Asp Leu Ala Ser Ile Glu Gly Ile Trp Thr Leu Asn Gly Arg Arg Asn	
88		270 275 280
89	gat cca gag aca ctg gat ggt ctg gat gcg ctg agg gag ctg tgg cag	914
90	Asp Pro Glu Thr Leu Asp Gly Leu Asp Ala Leu Arg Glu Leu Trp Gln	
91		285 290 295 300
92	cta ttg ccc gtc acg gag ggt ctg tgt cca ctg ccg aac tgc ttt tac	962
93	Leu Leu Pro Val Thr Glu Gly Leu Cys Pro Leu Pro Asn Cys Phe Tyr	
94		305 310 315
95	gag ccg ggt acc tca ccg cag gag cag ctc ccc ttc att ata aat ttt	1010
96	Glu Pro Gly Thr Ser Pro Gln Glu Gln Leu Pro Phe Ile Ile Asn Phe	

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97          320          325          330
98  acc ttg tct cct aaa agc gca ctt ccc gaa cca cag atc tat ttc cct      1058
99  Thr Leu Ser Pro Lys Ser Ala Leu Pro Glu Pro Gln Ile Tyr Phe Pro
100          335          340          345
101  gct ttt ggg cag aac gac aaa acc atc gcg gaa gga ttg gcc acc ttc      1106
102  Ala Phe Gly Gln Asn Asp Lys Thr Ile Ala Glu Gly Leu Ala Thr Phe
103          350          355          360
104  ttt gag agc aga ggt tgg ggt ggc ttg gct aag agc tat cca gcg gat      1154
105  Phe Glu Ser Arg Gly Trp Gly Gly Leu Ala Lys Ser Tyr Pro Ala Asp
106          365          370          375          380
107  ttg gca tcc tac tat ccc gat gtg gac ctg cag acc gca aat cac ctg      1202
108  Leu Ala Ser Tyr Tyr Pro Asp Val Asp Leu Gln Thr Ala Asn His Leu
109          385          390          395
110  cag gcg tgg atc tcc ttc tct tac aag ggg aaa aaa ccg tac atg agt      1250
111  Gln Ala Trp Ile Ser Phe Ser Tyr Lys Gly Lys Lys Pro Tyr Met Ser
112          400          405          410
113  gtg tac ctc cat acc ttc gaa gcg ttc agt gct gct gcc cag gag gtg      1298
114  Val Tyr Leu His Thr Phe Glu Ala Phe Ser Ala Ala Ala Gln Glu Val
115          415          420          425
116  gct atg tgt cac gat ggc cac aat cct tag gactagttaa tcccttcatt      1348
117  Ala Met Cys His Asp Gly His Asn Pro *
118          430          435
119  ctatgcattcc gttgaatgtg ttggtcgaaa aaaaaaaaaa aaaaaa      1393
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122 <211> LENGTH: 437
123 <212> TYPE: PRT
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Primer 5956
127 <400> SEQUENCE: 2
128  Met Glu Ile Ser Lys Lys Ala Ala Thr Leu Leu Pro Lys Pro Phe Tyr
129    1          5          10          15
130  Val Leu Ser Gln Ala Leu Asn Leu Ser Asn Lys Asp His Thr Lys Trp
131          20          25          30
132  Trp Tyr Ser Thr Ala Pro Met Phe Ala Thr Met Met Ala Gly Ala Gly
133          35          40          45
134  Tyr Asp Val His Ala Gln Tyr Lys Phe Leu Cys Ile His Arg Glu Val
135          50          55          60
136  Ile Ile Pro Ala Leu Gly Pro Tyr Pro Glu Lys Gly Gln Pro Met His
137          65          70          75          80
138  Trp Lys Ser His Leu Thr Arg Phe Gly Leu Pro Phe Glu Leu Ser Phe
139          85          90          95
140  Asn Tyr Ser Lys Ser Leu Leu Arg Phe Ala Phe Glu Pro Leu Gly Ser
141          100          105          110
142  Leu Thr Gly Thr Lys Asp Asp Pro Phe Asn Thr Gln Ala Ile Arg Pro
143          115          120          125
144  Val Leu Gln Asp Leu Lys Ala Met Val Pro Gly Leu Asp Leu Glu Trp
145          130          135          140
146  Phe Asp His Phe Thr Lys Ala Leu Val Val Ser Glu Glu Glu Ala Arg

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147      145      150      155      160
148      Thr Leu Leu Asp Arg Asp Ile Glu Ile Pro Val Phe Lys Thr Gln Asn
149      165      170      175
150      Lys Leu Ala Ala Asp Leu Glu Pro Ser Gly Asp Ile Val Leu Lys Thr
151      180      185      190
152      Tyr Ile Tyr Pro Arg Ile Lys Ser Ile Ala Thr Gly Thr Pro Lys Glu
153      195      200      205
154      Arg Leu Met Phe Asp Ala Ile Lys Ala Ala Asp Lys Phe Gly Lys Val
155      210      215      220
156      Ala Thr Pro Leu Ala Ile Leu Glu Glu Phe Ile Ala Glu Arg Ala Pro
157      225      230      235      240
158      Thr Leu Leu Gly His Phe Leu Ser Cys Asp Leu Val Lys Pro Ser Glu
159      245      250      255
160      Ser Arg Ile Lys Val Tyr Cys Met Glu Arg Gln Leu Asp Leu Ala Ser
161      260      265      270
162      Ile Glu Gly Ile Trp Thr Leu Asn Gly Arg Arg Asn Asp Pro Glu Thr
163      275      280      285
164      Leu Asp Gly Leu Asp Ala Leu Arg Glu Leu Trp Gln Leu Leu Pro Val
165      290      295      300
166      Thr Glu Gly Leu Cys Pro Leu Pro Asn Cys Phe Tyr Glu Pro Gly Thr
167      305      310      315      320
168      Ser Pro Gln Glu Gln Leu Pro Phe Ile Ile Asn Phe Thr Leu Ser Pro
169      325      330      335
170      Lys Ser Ala Leu Pro Glu Pro Gln Ile Tyr Phe Pro Ala Phe Gly Gln
171      340      345      350
172      Asn Asp Lys Thr Ile Ala Glu Gly Leu Ala Thr Phe Phe Glu Ser Arg
173      355      360      365
174      Gly Trp Gly Gly Leu Ala Lys Ser Tyr Pro Ala Asp Leu Ala Ser Tyr
175      370      375      380
176      Tyr Pro Asp Val Asp Leu Gln Thr Ala Asn His Leu Gln Ala Trp Ile
177      385      390      395      400
178      Ser Phe Ser Tyr Lys Gly Lys Lys Pro Tyr Met Ser Val Tyr Leu His
179      405      410      415
180      Thr Phe Glu Ala Phe Ser Ala Ala Ala Gln Glu Val Ala Met Cys His
181      420      425      430
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183      435
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187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: Primer 5956
191 <400> SEQUENCE: 3
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196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence

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198 <220> FEATURE:  
199 <223> OTHER INFORMATION: Primer 5955  
200 <400> SEQUENCE: 4  
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203 <210> SEQ ID NO: 5  
204 <211> LENGTH: 20  
205 <212> TYPE: DNA  
206 <213> ORGANISM: Artificial Sequence  
207 <220> FEATURE:  
208 <223> OTHER INFORMATION: Primer 6120  
209 <400> SEQUENCE: 5  
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212 <210> SEQ ID NO: 6  
213 <211> LENGTH: 20  
214 <212> TYPE: DNA  
215 <213> ORGANISM: Artificial Sequence  
216 <220> FEATURE:  
217 <223> OTHER INFORMATION: Primer 6121  
218 <400> SEQUENCE: 6  
219 ccatatcttc tcagtctcca 20

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/099,704

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TIME: 15:54:00

Input Set : N:\Crf3\RULE60\10099704.raw

Output Set: N:\CRF3\04162002\J099704.raw